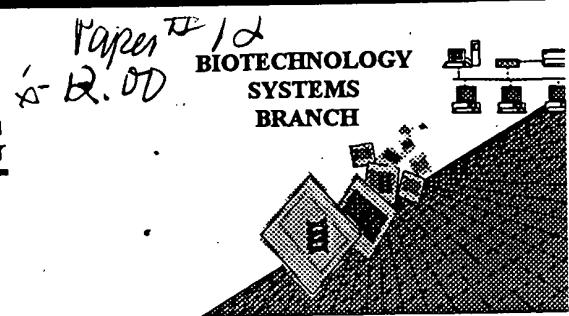


Violent

RAW SEQUENCE LISTING

ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/147,443A

Art Unit / Team No. 1644

Date Processed by STIC: 6/9/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

De Cloony

RAW SEQUENCE LISTING DATE: 06/09/2000
 PATENT APPLICATION: US/09/147,443A TIME: 17:01:44

Input Set : A:\09 147,443 SEQUENCE LISTING.txt
 Output Set: N:\CRF3\06082000\I147443A.raw

4 (1) GENERAL INFORMATION:
 E--> 6 (i) APPLICANT:
 14 (ii) TITLE OF INVENTION: Recombinant Fab-fragment with reactivity
 15 against Rhesus D antigens, DNA encoding them, complete
 16 antibodies comprising the Fab fragments and process for
 17 their preparation
 19 (iii) NUMBER OF SEQUENCES: 64
 E--> 0 (iv) CORRESPONDENCE ADDRESS:
 9 (B) STREET: Wankdorfstrasse 10
 10 (C) CITY: Bern 22
 11 (E) COUNTRY: Switzerland
 C--> 12 (F) ZIP: CH-3000
 C--> 21 (v) COMPUTER READABLE FORM:
 22 (A) MEDIUM TYPE: Floppy disk
 23 (B) COMPUTER: IBM PC compatible
 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 C--> 27 (vi) CURRENT APPLICATION DATA:
 C--> 28 (A) APPLICATION NUMBER: US/09/147,443A
 C--> 0 (B) FILING DATE: 21-Jan-1999
 C--> 29 (vii) PRIOR APPLICATION DATA:
 30 (A) APPLICATION NUMBER: EP 96810421.6
 31 (B) FILING DATE: 24-JUN-1996
 C--> 0 (viii) ATTORNEY/AGENT INFORMATION:
 7 (A) NAME: Rotkreuzstiftung Zentrallaboratorium
 8 Blutspendedienst

*Does Not Comply
 Corrected Diskette Needed*

All last page

ERRORED SEQUENCES

1110 (2) INFORMATION FOR SEQ ID NO: 21:
 1112 (i) SEQUENCE CHARACTERISTICS:
 1113 (A) LENGTH: 375 base pairs
 1114 (B) TYPE: nucleic acid
 1115 (C) STRANDEDNESS: single
 1116 (D) TOPOLOGY: linear
 1118 (ii) MOLECULE TYPE: cDNA to mRNA
 1120 (iii) HYPOTHETICAL: NO
 1122 (iv) ANTI-SENSE: NO
 1124 (v) FRAGMENT TYPE: N-terminal
 1126 (vi) ORIGINAL SOURCE:
 1127 (A) ORGANISM: Homo sapiens
 1128 (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 1129 (E) HAPLOTYPE: diploid
 1130 (G) CELL TYPE: Peripheral lymphocyte B
 1132 (vii) IMMEDIATE SOURCE:
 1133 (A) LIBRARY: cDNA LIBRARY, LD2

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/147,443A

DATE: 06/09/2000
TIME: 17:01:45

Input Set : A:\09 147,443 SEQUENCE LISTING.txt
Output Set: N:\CRF3\06082000\I147443A.raw

1134 (B) CLONE: LD2-1
1136 (viii) POSITION IN GENOME:
1137 (A) CHROMOSOME SEGMENT: chromosome 14
1138 (B) MAP POSITION: q32.3
1139 (C) UNITS: Chromosome band number
1141 (ix) FEATURE:
1142 (A) NAME/KEY: CDS
1143 (B) LOCATION: 1..375
1144 (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
1146 (ix) FEATURE:
1147 (A) NAME/KEY: CDR1, CDR2, CDR3
1148 (B) LOCATION: join(91..105, 148..198, 295..342)
1151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

E--> 1154 CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48
E--> 1155 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly 15
1156 1 5 10 15
E--> 1158 TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT 96
1159 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20
1160 20 25 30
E--> 1162 GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG 144
1163 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35
1164 35 40 45
E--> 1166 GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG 192
1167 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60
1168 50 55 60
E--> 1170 AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG GTC TAT 240
1171 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 65 70 75 80
1172 65 70 75 80
E--> 1174 CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC ACG GCT GTA TAT TAT TGT 288
1175 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys 85 90 95
1176 85 90 95
E--> 1178 GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC AAC TAT TAC CTG 336
1179 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 100 105 110
1180 100 105 110
E--> 1182 GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA, 375
1183 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125
1184 115

→ delete

VERIFICATION SUMMARY DATE: 06/09/2000
PATENT APPLICATION: US/09/147,443A TIME: 17:01:46

Input Set : A:\09 147,443 SEQUENCE LISTING.txt
Output Set: N:\CRF3\06082000\I147443A.raw

L:12 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
L:21 M:220 C: Keyword misspelled or invalid format, [(v) COMPUTER READABLE FORM:]
L:27 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:6 M:200 E: Mandatory Header Field missing, [(i) APPLICANT:] Value not provided
L:0 M:200 E: Mandatory Header Field missing, [(A) ADDRESSEE:]
L:0 M:200 E: Mandatory Header Field missing, [(D) STATE:]
L:0 M:248 E: Inserted missing Mandatory Header Field, [(iv) CORRESPONDENCE ADDRESS:]
L:0 M:247 C: Inserted Optional Header Field, [(viii) ATTORNEY/AGENT INFORMATION:]
L:0 M:249 C: Inserted Mandatory Field, [(B) FILING DATE:]
L:1152 M:254 E: No. of Bases conflict, Input:0 Counted:0 SEQ:21
L:1152 M:320 E: (1) Wrong Nucleic Acid Designator, 1
M:254 Repeated in SeqNo=21
L:1184 M:204 E: No. of Bases differ, LENGTH:Input:375 Counted:376 SEQ:21
L:1817 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:33
L:1821 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:33
L:1825 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:33
L:1829 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:33
L:2016 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:37
L:2668 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:2672 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:2676 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:2680 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:2684 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:2688 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:2903 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53